

# SEQUENCE LISTING

<110> Ruan, Yong-Ling  
Furbank, Robert T.  
Danny, Llewellyn J.

<120> Modification of sucrose synthase gene expression in plant tissue and uses therefor

<130> GHSUSY W01

<150> 60/251852  
<151> 2000-12-08

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<170> PatentIn version 3.1

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gat gag acc ctt ctt gct cac agg aac gag att ttg gcc ttg ctc tca	96
Asp Glu Thr Leu Leu Ala His Arg Asn Glu Ile Leu Ala Leu Leu Ser	
20 25 30	
agg atc gag ggc aaa gga aaa gga att ctg caa cac cat caa att att	144
Arg Ile Glu Gly Lys Gly Lys Gly Ile Leu Gln His His Gln Ile Ile	
35 40 45	
cta gag ttt gaa gct atc cct gaa gag aac aga aag aag ctc gct aat	192
Leu Glu Phe Glu Ala Ile Pro Glu Glu Asn Arg Lys Lys Leu Ala Asn	
50 55 60	
ggg gca ttt ttt gaa gta ttg aag gct agt cag gaa gcg atc gtg ttg	240
Gly Ala Phe Phe Glu Val Leu Lys Ala Ser Gln Glu Ala Ile Val Leu	
65 70 75 80	
cct cca tgg gtt gca ctt gct gtt cgt cca agg cct ggt gtt tgg gag	288
Pro Pro Trp Val Ala Leu Ala Val Arg Pro Arg Pro Gly Val Trp Glu	

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aga ctt ctt cct gat gct gtc gga aca tgc ggt caa cga ctt gag Arg Leu Leu Pro Asp Ala Val Gly Thr 345 Thr Cys Gly Gln Arg Leu Glu 350	1056
aaa gta tac gga aca gag cac tcg gat att ctt cga gta ccc ttc aga Lys Val Tyr Gly Thr Glu His Ser Asp 360 Ile Leu Arg Val Pro Phe Arg 365	1104
aca gaa aag gga att gtt cga aaa tgg atc tca aga ttt gaa aaa gtc Thr Glu Lys Gly Ile Val Arg Lys Trp 375 Ile Ser Arg Phe Glu Lys Val 380	1152
tgg cca tac ttg gaa acc tac aca gag gat gtt gct cat gaa atc tcc Trp Pro Tyr Leu Glu Thr Tyr Thr Glu Asp 395 Val Ala His Glu Ile Ser 400	1200
aaa gag ttg cac ggc acg cca gat ctg atc atc gga aac nac agc gac Lys Glu Leu His Gly 405 Leu Thr Pro Asp Leu Ile Ile Gly Asn Xaa Ser Asp 415	1248
ggc aat atc gtc gcc tcc ttg ctc gca cat aaa tta ggt gtc aca cag Gly Asn Ile Val Ala Ser Leu Leu Ala His Lys Leu Gly Val Thr Gln 420 425 430	1296
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aca gct gat ctt ttt gca atg aac cat aca gat ttc atc atc acc agt Thr Ala Asp Leu Phe Ala Met Asn His Thr Asp 475 Phe Ile Ile Thr Ser 480	1440
act ttc cag gaa att gca gga agc aag gac act gtt ggt caa tac gag Thr Phe Gln Glu Ile 485 Ala Gly Ser Lys Asp Thr Val Gly Gln Tyr Glu 495	1488
agc cac act gct ttc act ctt cct ggt ctc tac cgt gtt gta cat ggt Ser His Thr Ala Phe Thr Leu Pro Gly 505 Leu Tyr Arg Val Val His Gly 510	1536
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ttc cat cct gag atc gaa gac ctt ctt tac acc aaa gtt gag aat gaa Phe His Pro Glu Ile Glu Asp Leu Leu Tyr Thr Lys Val Glu Asn Glu	1680



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ggt cca ttg gca gag gag taa att gaa cct gtt aaa taa cat tgg gcc	2448
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Gly Phe Ser Trp Arg Ile Ile Phe Cys Phe Val Ile Ser Ile Gly Glu	
815 820 825 830	
gct cct ttg tat ttc atc ttg tct ttt cct ttt cct ttt ttc gcc gcc	2544
Ala Pro Leu Tyr Phe Ile Leu Ser Phe Pro Phe Phe Ala Gly	
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Ile Val Thr Trp Gly Cys Ala Pro Val Asn Ser Ser Ile Trp	
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Arg Ile Glu Gly Lys Gly Lys Gly Ile Leu Gln His His Gln Ile Ile	
35 40 45	
Leu Glu Phe Glu Ala Ile Pro Glu Glu Asn Arg Lys Lys Leu Ala Asn	
50 55 60	

Gly Ala Phe Phe Glu Val Leu Lys Ala Ser Gln Glu Ala Ile Val Leu  
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Pro Pro Trp Val Ala Leu Ala Val Arg Pro Arg Pro Gly Val Trp Glu  
85 90 95

Tyr Ile Arg Val Asn Val His Ala Leu Val Val Glu Glu Leu Thr Val  
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Ala Glu Tyr Leu His Phe Lys Glu Glu Leu Val Asp Gly Ser Ser Asn  
115 120 125

Gly Asn Phe Val Leu Glu Leu Asp Phe Glu Pro Phe Asn Ser Ser Phe  
130 135 140

Pro Arg Pro Thr Leu Ser Lys Ser Ile Gly Asn Gly Val Glu Phe Leu  
145 150 155 160

Asn Arg His Leu Ser Ala Lys Leu Phe His Asp Lys Glu Ser Met His  
165 170 175

Pro Leu Leu Glu Phe Leu Arg Val His Cys His Lys Gly Lys Asn Met  
180 185 190

Met Leu Asn Asp Arg Ile Gln Asn Leu Asn Ala Leu Gln His Val Leu  
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Arg Lys Ala Glu Glu Tyr Leu Gly Thr Leu Pro Pro Glu Thr Pro Cys  
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Ala Glu Phe Glu His Arg Phe Gln Glu Ile Gly Leu Glu Arg Gly Trp  
225 230 235 240

Gly Asp Thr Ala Glu Arg Val Leu Glu Met Ile Gln Leu Leu Leu Asp  
245 250 255

Leu Leu Glu Ala Thr Asp Pro Cys Thr Leu Glu Lys Phe Leu Gly Arg  
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Ile Pro Met Val Phe Asn Val Val Ile Leu Thr Pro His Gly Tyr Phe  
275 280 285

Ala Gln Asp Asn Val Leu Gly Tyr Pro Asp Thr Gly Gly Gln Val Val  
290 295 300

Tyr Ile Leu Asp Gln Val Arg Ala Leu Glu Asn Glu Met Leu Leu Arg  
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Ile Lys Gln Gln Gly Leu Asn Ile Thr Pro Arg Ile Leu Ile Ile Thr  
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Arg Leu Leu Pro Asp Ala Val Gly Thr Thr Cys Gly Gln Arg Leu Glu  
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Lys Glu Leu His Gly Thr Pro Asp Leu Ile Ile Gly Asn Xaa Ser Asp  
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Gly Asn Ile Val Ala Ser Leu Leu Ala His Lys Leu Gly Val Thr Gln  
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Cys Thr Ile Ala His Ala Leu Glu Lys Thr Lys Tyr Pro Asp Ser Asp  
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Ile Asp Val Phe Asp Pro Lys Phe Asn Ile Val Ser Pro Gly Ala Asp  
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Met Glu Ile Tyr Phe Pro Tyr Thr Glu Glu Lys Arg Arg Leu Lys His  
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Phe His Pro Glu Ile Glu Asp Leu Leu Tyr Thr Lys Val Glu Asn Glu  
545 550 555 560

Glu His Leu Cys Val Leu Asn Asp Arg Asn Lys Pro Ile Leu Phe Thr  
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Met Pro Arg Leu Asp Arg Val Lys Asn Leu Thr Gly Leu Val Glu Trp  
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Cys Gly Lys Asn Pro Lys Leu Arg Glu Leu Ala Asn Leu Val Val Val  
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Gly Gly Asp Arg Arg Lys Glu Ser Lys Asp Leu Glu Glu Lys Ala Glu  
610 615 620

Met Lys Lys Met Phe Glu Leu Ile Asp Lys Tyr Asn Leu Asn Gly Gln  
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Phe Arg Trp Ile Ser Ser Gln Met Asn Arg Ile Arg Asn Val Glu Leu  
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Tyr Arg Tyr Ile Cys Asp Thr Lys Gly Ala Phe Val Gln Pro Ala Leu  
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Tyr Glu Ala Phe Gly Leu Thr Val Val Glu Ala Met Thr Cys Gly Leu  
675 680 685

Pro Thr Phe Ala Thr Cys Asn Gly Gly Pro Ala Glu Ile Ile Val His  
690 695 700

Gly Lys Ser Gly Phe Asn Ile Asp Pro Tyr His Gly Asp Gln Ala Ala  
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Asp Ile Leu Val Asp Phe Phe Glu Lys Cys Lys Lys Asp Pro Ser His  
725 730 735

Trp Asp Lys Ile Ser Gln Gly Gly Leu Lys Arg Ile Glu Glu Lys Tyr  
740 745 750

Thr Trp Lys Ile Tyr Ser Glu Arg Leu Leu Thr Leu Thr Gly Val Tyr  
755 760 765



Gly Phe Trp Lys His Val Ser Asn Leu Glu Arg Arg Glu Ser Arg Arg  
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Phe Ala Gly Ile Val  
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